AMENDMENT

In the Claims

Please cancel claims 128-145 without prejudice or disclaimer. Please enter the following new claims 146-161:

146. (New) A method for making a peptide which comprises an HLA-A2.1 restricted T cell binding motif, said binding motif consisting of 9-10 amino acid residues, and wherein said peptide binds an HLA-A2.1 molecule, said method comprising the steps of

(a) providing an amino acid sequence of an antigen of interest;

(b) identifying within said sequence a subsequence consisting of 9-10 amino acid residues which subsequence has a first amino acid anchor at position 2 of said subsequence selected from the group consisting of L, M, I, V, A and T and a second amino acid anchor residue at the C-terminus of said subsequence selected from the group consisting of A and M; or

which subsequence has a first amino acid anchor at position 2 of said subsequence selected from the group consisting of I, V, A and T and a second amino acid anchor residue at the C-terminus of said subsequence selected from the group consisting of L, V, I, A and M;

(c) identifying a fragment of said antigen which contains a subsequence identified in step (b); and

(d) preparing a peptide which contains said fragment.

147. (New) The method of claim 146, wherein said subsequence consists of 9 amino acid residues and wherein

position 1 of said subsequence is not an amino acid selected from the group consisting of D, E and P, or

position 3 or 7 of said subsequence is not an amino acid selected from the group consisting of D, E, R, K and H, or

position 6 of said subsequence is not an amino acid selected from the group consisting of R, K and H.

148. (New) The method of claim 147, wherein

position 1, 3 or 5 of said subsequence is selected from the group consisting of Y, F and W, or

position 4 of said subsequence is selected from the group consisting of S, T and C, or

position 7 of said subsequence is A.

149. (New) The method of claim 146, wherein the subsequence consists of 10 amino acid residues, and wherein

position 1 of said subsequence is not an amino acid selected from the group consisting of D, E and P, or

position 3 of said subsequence is not an amino acid selected from the group consisting of D and E, or

position 4 of said subsequence is not an amino acid selected from the group consisting of R, K, H and A, or

position 5 of said subsequence is not P, or

position 7 of said subsequence is not an amino acid selected from the group consisting of R, K and H, or

position 8 of said subsequence is not an amino acid selected from the group consisting of D, E, R, K and H, or

position 9 of said subsequence is not an amino acid selected from the group consisting of R, K and H.

150. (New) The method of claim 149, wherein

position 1 of said subsequence is selected from the group consisting of A, Y, F and W, or

position 3 of said subsequence is selected from the group consisting of L, V, I and M, or

position 4 of said subsequence is G, or

position 8 of said subsequence is selected from the group consisting of Y, F, W, L, V, I and M.

151. (New) The method of claim 146, wherein said peptide consists of 9-10 amino acids.

152. (New) The method of claim 151, which further comprises assessing the ability of said fragment to bind an HLA-A2.1 molecule to identify at least one fragment which successfully binds said HLA-A2.1 molecule.

153. (New) The method of claim 152, which further comprises testing for said peptide's ability to be recognized by HLA-A2.1 cytotoxic T cells or to stimulate a cytotoxic T cell response.

154. (New) A method to design a peptide which consists of less than 15 amino acids and which peptide comprises a subsequence consisting of 9-10 amino acids which binds an HLA-A2.1 molecule which method comprises

(a) providing an amino acid sequence of an antigen of interest;

(b) identifying within said sequence an amino acid subsequence consisting of 9-10 amino acid residues which subsequence has a first amino acid anchor at position 2 of said subsequence selected from the group consisting of L, M, I, V, A and T and a second amino acid anchor at the C-terminus of said subsequence selected from the group consisting of A and M; or

which subsequence has a first amino acid anchor at position 2 of said subsequence selected from the group consisting of I, V, A and T and a second amino acid anchor at the C-terminus of said subsequence selected from the group consisting of L, V, I, A and M;

(c) identifying a fragment of said antigen which contains a subsequence identified in step (b); and

(d) designing a peptide which comprises said fragment.

155. (New) A peptide designed by the method of claim 154, wherein the peptide consists of 9-10 amino acids.

156. (New) The method of claim 154, wherein said subsequence consists of 9 amino acid residues and wherein

position 1 of said subsequence is not an amino acid selected from the group consisting of D, E and P, or

position 3 or 7 of said subsequence is not an amino acid selected from the group consisting of D, E, R, K and H, or

position 6 of said subsequence is not an amino acid selected from the group consisting of R, K and H.

157. (New) The method of claim 156, wherein

position 1, 3 or 5 of said subsequence is selected from the group consisting of Y, F and W, or

position 4 of said subsequence is selected from the group consisting of S, T and C, or

position 7 of said subsequence is A.

158. (New) The method of claim 154, wherein the subsequence consists of 10 amino acid residues, and wherein

position 1 of said subsequence is not an amino acid selected from the group consisting of D, E and P, or

position 3 of said subsequence is not an amino acid selected from the group consisting of D and E, or

position 4 of said subsequence is not an amino acid selected from the group consisting of R, K, H and A, or

position 5 of said subsequence is not P, or

position 7 of said subsequence is not an amino acid selected from the group consisting of R, K and H, or

position 8 of said subsequence is not an amino acid selected from the group consisting of D, E, R, K and H, or

position 9 of said subsequence is not an amino acid selected from the group consisting of R, K and H.

159. (New) The method of claim 158, wherein

position 1 of said subsequence is selected from the group consisting of A, Y, F and W, or

position 3 of said subsequence is selected from the group consisting of L, V, I and M, or

position 4 of said subsequence is G, or

position 8 of said subsequence is selected from the group consisting of Y, F, W, L, V, I and M.

160. (New) An isolated peptide of less than 15 amino acids and which comprises an HLA-A2.1 binding motif of 9-10 amino acids in length;

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is I, and a second amino acid anchor at the C-terminus of said motif which is V, I, A or M; or

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is V, and a second amino acid anchor at the C-terminus of said motif which is L, V, I or M; or

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is A, and a second amino acid anchor at the C-terminus of said motif which is L, V or M; or

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is T, and a second amino acid anchor at the C-terminus of said motif which is L, I or M; or

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is L, and a second amino acid anchor at the C-terminus of said motif which is M; or

wherein said binding motif has a first amino acid anchor at position 2 of said motif which is M, and a second amino acid anchor at the C-terminus of said motif which is A or M; and

wherein a peptide that consists of said binding motif elicits a CTL response when complexed with said HLA-A2.1 molecule.

161. (New) An isolated peptide of claim 160, wherein said peptide has the sequence KVAELVHFL.